Placental transcriptomes in the common aneuploidies reveal critical regions on the trisomic chromosomes and genome-wide effects.

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Public Summary:
OBJECTIVE: Chromosomal aberrations are frequently associated with birth defects and pregnancy losses. Trisomy 13, Trisomy 18 and Trisomy 21 are the most common, clinically relevant fetal aneusomies. This study used a transcriptomics approach to identify the molecular signatures at the maternal-fetal interface in each aneuploidy. METHODS: We profiled placental gene expression (13-22 weeks) in T13 (n = 4), T18 (n = 4) and T21 (n = 8), and in euploid pregnancies (n = 4). RESULTS: We found differentially expressed transcripts (>/=2-fold) in T21 (n = 160), T18 (n = 80) and T13 (n = 125). The majority were upregulated and most of the misexpressed genes were not located on the relevant trisomic chromosome, suggesting genome-wide dysregulation. A smaller number of the differentially expressed transcripts were encoded on the trisomic chromosome, suggesting gene dosage. In T21, <10% of the genes were transcribed from the Down syndrome critical region (21q21-22), which contributes to the clinical phenotype. In T13, 15% of the upregulated genes were on the affected chromosome (13q11-14), and in T18, the percentage increased to 24% (18q11-22 region). CONCLUSION: The trisomic placental (and possibly fetal) phenotypes are driven by the combined effects of genome-wide phenomena and increased gene dosage from the trisomic chromosome. (c) 2016 John Wiley & Sons, Ltd.

Scientific Abstract:
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